

Db	235	QKAATEPKPVPVKPPAP---	EPEPVATE-----	EVQPAAE-----		
Qy	231	DKKKKGKEKEKE-KKKGSKATVKAMOEALAKLKEEEROKREBERIKRLEELE	287			
Db	279	GKKDKRAPEEKKADKKKGMSASVAAWQEQRKRKEERLEREEAERIRLEDERE	336			
RESULT	5					
Q9NJH7						
ID	Q9NJH7	PRELIMINARY;	PRT;	1144 AA.		
AC	Q9NJH7;					
DT	01-OCT-2000 (TReMBLrel. 15, Created)					
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)					
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)					
DE	IF2 PROTEIN					
GN	CIF2 OR GG10840.					
OS	Drosophila melanogaster (Fruit fly).					
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
OX	Ephydroidea; Drosophilidae; Drosophila.					
NCBI_TaxID=7227;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE-20142670; PubMed-10678180;					
RA	Carrera P., Johnstone O., Nakamura A., Casanova J., Jackle H.,					
RA	Lasko P.;					
RT	"VASA mediates translation through interaction with a Drosophila yfF2					
RT	homolog,";					
RL	Mol. Cell 5:181-187(2000).					
DR	EMBL; AF143207; AAF36532.1; -.					
DR	FlyBase; FBgn0026259; CIF2.					
DR	InterPro; IPR000795; GTP_EFTU.					
DR	InterPro; IPR000178; IF2.					
DR	PRINTS; PR00315; ELONGATNFCT.					
KW	GTP-binding; Protein biosynthesis.					
SQ	SEQUENCE 1144 AA; 127203 MW; A035415A376ZCF0C CRC64;					
Query Match	21.5%;	Score 315;	DB 5;	Length 1144;		
Best Local Similarity	30.3%;	Pred. No. 1.le-09;				
Matches	92;	Conservative 61;	Mismatches 97;	Indels 54;	Gaps	
Qy	11 KRDRRAKKSFDONDSLEELEDKSDSKKTAKPKVEMYSGDDDDO-----	56				
Db	60 KKLNVCKGKAGNDSDSEVVYPAGKASKKSAFELMLDDDDQDPAQESOSEEEKV	119				
Qy	57 FNKLPPKAKGACKSNKKWDGSEEDNSKKIKERSINSSGSG-----	DESDE 106				
Db	120 VSKPQKNKKKKKAKRK--GKDDDEDLDKVLAELQAQYAGEAAPATTVVSPEELADE	177				
Qy	107 FLSRKGOKKNOKPCPNI--ESGNEDDDASFKITVAQKKAERKKRDEEKAKL	164				
Db	178 FSKKKNNKQAKAAVAENAGEDASDDEGGSTVSAQQKKKKERQ--KREAALA--	233				
Qy	165 RLKKEBELETGTGKDQSQRKSFEEETVTSKVTDTCVIPASEKAEPTPTAAADDNE	224				
Db	234 ----KOKATEPKPVEKPAP---EPEPVATE----EVQPAAE-----	EEKS 272				
Qy	225 GDKKKDKKKKKEBEKE-KKKGPSKATVKAMOEALAKLKEEBEROKREBERIKRL	283				
Db	273 SKNKKGKDKDAEPBEEKKDAKKKGMSASVAAWOQLKRKEEBERLEREEAERIRLE	332				
Qy	284 EELE 287					
Db	333 DERE 336					
RESULT	6					
Q18401						
ID	Q18401	PRELIMINARY;	PRT;	390 AA.		
AC	Q18401;					
DT	01-NOV-1996 (TReMBLrel. 01, Created)					


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Db 157 KKH-----EDVSQKELEEDPGKNNKKKEKD-----ESCTEE-----KKKKPKKEKKQ 200
Qy 151 EREKKRDEKAKRLK-KKEELETGKKDQSKQB-----SQRKFEETVSKVTVDTGCV 205
Db 201 KEEKSNEDEKVKGKEKEGKGLDLE--KEDEKKKEHDETDQEMKESKKNK-----251
Qy 206 IPASEEKAETPTAAEDDNGDKKKDK-----KKKKGKEKEKEB-KKKGPS 251
Db 252 ---KKEDES-CAEKKKKPKDKEKKEKDESTEKEDKKLGGKKGKPKEDGKKTKEH 307
Qy 252 KATVKAQALAKLKEEERQKREER-----IKRLEELESK 289
Db 308 DATEQEMDDEAADHKEGKKKKNNKDKAKKKTETVIDEVEKETK 349

RESULT 11
Q95XW8 PRELIMINARY; PRT; 679 AA.
AC Q95XW8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 77.9 KDA PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Smith A., Wohldmann P.;
RT "The sequence of C. elegans cosmid Y55B1BR.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024824; AAK8503.1; -
KW Hypothetical protein.
SQ SEQUENCE 679 AA; 77907 MW; 6B3F259D7C4AB02C CRC64;

Query Match 19.2%; Score 281; DB 5; Length 679;
Best Local Similarity 27.5%; Pred. No. 4.8e-08;
Matches 98; Conservative 67; Mismatches 112; Indels 80; Gaps 14;

Qy 7 OKTKKRRRAKQSFDDNSE-----ELEDKDSKSKTAKPKVEMYSGSDDDDDFN 58
Db 232 KWKNNKAKRSKDDSDSDSEMERRRKKSKSKSKFKRKRKRVAVNDSDDEE 291
Qy 59 KLPKKAKQAQSKNNKWDGSEEDNSKKIKERSINSSGESDESDEFQSRKQG--- 114
Db 292 EKPEKRSKSKKA--VIDSSSEDEEEKSKRSK-----KSKESDEQAQSDSEEVV 344
Qy 115 --KKNQKN-----KCPNITESNEDDDASFKTKT--VAQKKAERERERKKRDEE 160
Db 345 EVKKNKSPKTKPKTKAVKESEESDEEEVVKKKSKINKRKAKESSSDSEEEVEE 404
Qy 161 KAKLR-KLKEKEELETGKKDQSKOKESORKEET-----VKSKVTVDTGVIPASEEKA 214
Db 405 SPKKTKSPKRSKSKAAKESEESDNEEEVEVDYSPKKVKSPKSKSKPAKVESE 464
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Qy 215 TPTAAEDDNEGDK---KKDKKKK-----GEKEEKE---KKG--PS 251
Db 465 EPSDNEEEVEESPICKDKTPRYSRKAARVESTESSGNEEEVEESPCKKGTPT 524
Qy 252 KATVK--AMQALAKLKEEERQKR-----EEERIKRLEELESKP 290
Db 525 KSKKSAAVEEDNEEDVEESFPKRTSPRKSCKKRAAKESEESDNEVEEDSP 581

RESULT 12
Q9LGS9 PRELIMINARY; PRT; 260 AA.
AC Q9LGS9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 3, BAC CLONE:FLD9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural Analysis of Arabidopsis thaliana Chromosome 3. III.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002460; BAA97098.1; -
DR InterPro; IP001386; Linker_histone.
DR PRINTS; PRO0624; HISTONEH5.
SQ SEQUENCE 260 AA; 33307 MW; 43E2394CB8131143 CRC64;

Query Match 19.1%; Score 279.5; DB 10; Length 260;
Best Local Similarity 25.3%; Pred. No. 2.6e-09;
Matches 71; Conservative 70; Mismatches 98; Indels 41; Gaps 3;

Qy 2 KRNSPQIKKKRRRAKQSFDDNSEEDKDSKSKTAKPKVEMYSGSDDDDDFNKL 61
Db 7 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK-----KKK 52
Qy 62 KKAQKAKSNKKWDGSEEDNSKKIKERSINSSGESDESDEFQSRKQKKNK 121
Db 53 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 112
Qy 122 PGPNIESGNEDDASFKTKTVAQKKAERERERKRRDEKAKLRKLEKEELETGKKDQ 181
Db 113 -----KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 156
Qy 182 KOKESORKEEETVSKVTVDTGVIPASEEKAETPTAAEDDNEGDKKKDKKKKGEKEE 241
Db 157 KKKKKKKKKKKKKKK-----KKKKKKKKKKKKKKKKKKKKKKKKKKKK 205
Qy 242 KEKEKKGPSKATVKAMQALAKLKEEERQKREERIKR 282
Db 206 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 246

RESULT 13
Q9SRD2 PRELIMINARY; PRT; 1280 AA.
AC Q9SRD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSLATION INITIATION FACTOR IF-2, 73082-68138.
GN F28016.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
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[1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA      Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA      Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT      "Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence.";
RL      Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AC010718; AAP04442.1; -
DR      InterPro: IPR000795; GTP_EFTU.
DR      InterPro: IPR004161; GTP_EFTU_D2.
DR      InterPro: IPR000178; IF2-
DR      Pfam: PF00009; GTP_EFTU; 1.
DR      Pfam: PF03144; GTP_EFTU_D2; 1.
DR      PRINTS; PR00315; ELONGATNFT.
DR      GTP-binding; Initiation factor; Protein biosynthesis.
SQ      GTP-binding; Initiation factor; BC1A2BF75A859D0C CRC64;
SQ      SEQUENCE 1280 AA; 140708 MW; 140708 MW; 140708 MW;

Query Match          18.8%; Score 276.5; DB 10; Length 1280;
Best Local Similarity 26.0%; Pred. No. 1.4e-07;
Matches 111; Conservative 59; Mismatches 100; Indels 157; Gaps 19;

QY      18 KKQSFDNDSEELDKSKKTAKPKVMYSG-----SDDDDF----- 57
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      30 KKAQIDDDDEYSIGTEUSEEESKVEEEKVVITGKKKGKGNKGTQDDDDFSDKVSAA 89
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      58 ---NKLP-----KKAQGKA-----QSNKKWDCGEDE-----DN 84
DB      :||::||::||::||::||::||::||::||::||::||::||::||
QY      90 GVRDDVPEIAFVGKKKSCKGGGSVFALLDDEDEDNEGDGKDDEPVISFGKKHA 149
DB      :||::||::||::||::||::||::||::||::||::||::||::||
QY      85 SKTIKE-----RSRINSSGESGDSDEFIQ-----SRGQKKKNQN----- 120
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      150 SKGKKGNGNSFAASAFDALGSDDDDTEVHDEDEEEESPITFSGKKKKSKSKKNTNSFT 209
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      121 -----KPGNIENED-----DDASFKITVAQKAERKE-----REKRKRDEEK 161
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      210 ADLLDEEGVDASNRDSENTIEDSESPVTFSGKKKSKKGGSVLASVGDDSVADETK 269
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      162 AKLRKLKEKELETKG-KDOOSKQESORKPFEETVKSVTVDGVIPAS-----EE 211
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      270 TS--DTKNVEVETGSKKKKKNNKNSORTVQEEDLDKLLAALGETPAERPASTPVEE 327
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      212 KAETPP-----TAAEDDNEG-----KKKKDKKKKKG-----KEEKEKE 245
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      328 KAAQPEVPAPVENAGEKEGEETAARKKKKKKKKEKEKAAAAAATSSVEVKEEQEE 387
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      246 -----KKKGSKAT-----VKAMQPALAKLKEEEEQRKEEERI-----KR 282
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      388 SVTEPLQPKKKDAKGKAEKKIPKHVREMOPALRRQEAERKEEKEEELURKEEEEE 447
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      283 LEELESK 289
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||
QY      448 QEELEAQ 454
DB      |||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 14
Q9SY6 PRELIMINARY; PRT; 1166 AA.
ID Q9SY6
AC Q9SY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F9H16.10 PROTEIN.
DE F9H16.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;

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RA	Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA	Altai H., Araujo R., Huizar K.L., Rowley D., Buehler E., Dunn P.,
RA	Gonzalez A., Kremenskaia I., Kim C., Lenz C., Li J., Liu S.,
RA	Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA	Walker M., Yu G., Ecker J., Theologis A., Davis R.W.
RL	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC	-!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
DR	EMBL; AC007369; AACD30599.1; -;
DR	HSP; Q58083; 1HV8.
DR	InterPro; IPRO01410; DEAD.
DR	InterPro; IPRO00629; DEAD_Atp_helicase.
DR	InterPro; IPRO01650; Helicase_C.
DR	Pfam; PF00270; DEAD; 1.
DR	Pfam; PF00271; helicase_C; 1.
DR	SMART; SM00487; DEXDC; 1.
DR	SMART; SM00490; HELIC; 1.
DR	PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW	Atp-binding; Helicase; RNA-binding
SQ	SEQUENCE 1166 AA; 133033 MW; 597BD171F02666B95 CRC64;
Query Match 18.5%; Score 272; DB 10; Length 1166;	
Best Local Similarity 25.5%; Pred. No. 2.3e-07;	
Matches 77; Conservative 75; Mismatches 98; Indels 52; Gaps	
Qy	10 KKRKDRRAKKQSEDDNDSELEDKSKKTAKPKVEMYSGSDDDDFNKLPPKAKGKAQ 69 : : : : : : : : :
Dd	24 KSRRDRSRNERKKDGKGRREKDRKKRV-----KSSDSDDYDRDDDEEREK-- 73
Qy	70 KSNKKWDGSEDEDNSKKIKERSINSGSGESDESDE----FLQSRKGOKKNQKNKP 124 : : : : : : : : : : :
Dd	74 RKERERRRDRXVRKRSRKSSDSDDVDVEEDERKRRRYNEKERGHREHQR-GK 132
Qy	125 NIESGNDDDAASFKIKTVAAQKAEKREKRRKKDEEAKLRLLKEKEELETKKKDSK 184 : : : : : : : : : : : : : : :
Dd	133 DRKDRREBEKKUK-EREREKDRERREREEREKERVKERERREDGERDRREKER 191
Qy	185 ESORKFEETVKSVTYDTGVIPASEEKAETPTAAEDDNEDGKKKKKKKGEKEEKEEK 244 : : : : : : : : : : : : :
Dd	192 GSRRNRERSRE-----VGNEE-----SDDDVKRDLLK--RRKEGGERKEKER 233
Qy	245 EKKGK-----PSKATVKAMQALAKLKEEE---RQKREEE-----RTKRLLEELE 287 : : : : : : : : : : : :
Dd	234 EKSYSRSSRHEDSPKRSKSVNEDGEKKEKKTREELEDEQKKLDVEEKRRRRYQEWQELK 293
Qy	288 SK 289
Dd	294 RK 295
RESULT 15	
Q9DGL1	ID Q9DGL1 PRELIMINARY; PRT; 791 AA.
AC	Q9DGL1; 16, Created)
DT	01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DE	01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE	RETINITIS PIGMENTOSA CTSPA REGULATOR-LIKE PROTEIN (FRAGMENT).
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Tetraodontiformes; Percomorpha; Tetraodontiformes;
OX	NCBI_TaxID=31033;
RP	[1]
RN	SEQUENCE FROM N.A.
RA	Vervoort R., Lennon A., Bird A.C., Tulloch B., Axton R., Milano M.G.,
RA	Meindl A., Leintinger T., Ciccodicola A., Wright A.F.;
FT	"Mutational hot spot within a new RPGR exon in X-linked retinitis pigmentosa";
RT	Nat. Genet. 0:0-(2000).
FT	EMBL; AF286475; AAG00554.1; -;
NT	NON TER 1 1

